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Melvang, Heidi Mikkelsen; Grønbæk, Betina Chemnitz; Brogaard, Louise; Jakobsen, Jeanne Toft; Jungersen, Gregers

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Characterization of gene expression profiles to chronic infection with *Mycobacterium avium* subspecies *paratuberculosis*

Heidi Mikkelsen, Christina Chemnitz Grønbæk, Louise Brogaard, Jeanne T. Jakobsen and Gregers Jungersen
Technical University of Denmark, National Veterinary Institute, Section for Immunology and Vaccinology, Copenhagen, Denmark

Mycobacterium avium subsp. *paratuberculosis* (Map) causes paratuberculosis, a chronic enteritis of ruminants. The aim of the study was to use high-throughput reverse transcriptase (RT) qPCR to describe intestinal gene expression patterns in response to different levels of Map infection with a large panel of immunologically relevant genes.

For the study we selected samples of 6 calves that were all experimentally infected with Map at two weeks of age and based on serology, histology and Map tissue load were classified as protected (n=2) or unprotected (n=2) after vaccination, or un-vaccinated infected controls (n=2). From each calf, 7 intestinal tissue samples and 3 lymph node samples, collected at 10 months of age, were used for cDNA synthesis. Expression of a total of 37 selected genes including inflammatory, Th1 and Th17 related genes were explored.

The results showed that Map infection, as expected, leads to increased expression of local IFN-γ. Expression of IL-10 also increased as a result of Map infection, and this increase was more correlated to the amount of Map than IFN-γ, indicating a shift towards a regulatory environment as infection progress. Th17-mediated immune responses were suppressed at this stage. Gene expression of all other genes could not be interpreted in relation to infection status.

High throughput RT qPCR can be used for exploring gene expression patterns in response to Map infection but larger study groups are needed to fully understand which are key mechanisms and pathways responsible for protection or disease.